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<110> ProChon Biotech, Ltd.
MorphoSys AG
Yayon, Avner
Thomassen-Wolf, Elisabeth
Rom, Eran
Borges, Eric

<120> ANTIBODIES THAT BLOCK RECEPTOR PROTEIN TYROSINE KINASE ACTIVATION

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<141> 2003-12-15

<150> US 60/299,187
<151> 2001-06-20

<150> PCT/IL02/00494
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 <302> Fully synthetic human combinatorial antibody libraries (HuCAL)
 based on modular consensus frameworks and CDRs randomized with
 trinucleotides.
 <303> J Mol Biol
 <304> 296
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 <303> j mol biol
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tatccagtga	ttttttctc	cattttagct	tccttagctc	ctgaaaatct	cgataactca	3960
aaaaatacgc	ccggtagtga	tcttatttca	ttatggtaa	agttggaaacc	tcacccgacg	4020
tctaattgtga	gttagctcac	tcattaggca	cccaggctt	tacactttat	gcttccggct	4080
cgtatgtgt	gtggaattgt	gagcggataa	caatttcaca	cagggaaacag	ctatgaccat	4140
gattacgaat	t					4151

<210> 54
<211> 306
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<220>
<221> misc_feature
<222> (253)..(255)
<223> NNN=ACT OR GTT

<400> 54	60					
gatatccaga	tgacccagag	cccgtagc	ctgagcgcga	gcgtgggtga	tcgtgtgacc	60
attacctgca	gagcgagcca	gggcatttagc	agctatctgg	cgtggtagcca	gcagaaaccca	120
ggtaaagcac	cgaaaactatt	aatttatgca	gccagcagct	tgcaaagcgg	ggtcccgtcc	180
cgttttagcg	gctctggatc	cggcactgat	tttaccctga	ccattagcag	cctgcaacct	240
gaagactttg	cgnnttatta	ttgccagacc	tttggccagg	gtacgaaagt	tgaaattaaa	300
cgtacg						306

<210> 55
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<400> 55	60					
gatatccaga	tgacccagag	cccgtagc	ctgagcgcga	gcgtgggtga	tcgtgtgacc	60
attacctgca	gagcgagcca	gggcatttagc	agctatctgg	cgtggtagcca	gcagaaaccca	120
ggtaaagcac	cgaaaactatt	aatttatgca	gccagcagct	tgcaaagcgg	ggtcccgtcc	180
cgttttagcg	gctctggatc	cggcactgat	tttaccctga	ccattagcag	cctgcaacct	240
gaagactttg	cgttttatta	ttgcttcag	tatggttcta	ttcctcctac	cttggccag	300
ggtacgaaag	ttgaaattaa	acgtacg				327

<210> 56
 <211> 309
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> polynucleotide sequence of a VL domain

<220>
 <221> misc_feature
 <222> (256)..(258)
 <223> NNN=ACT OR GTT

<400> 56

gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccggcgaa acgtgcgacc	60
ctgagctgca gagcggccca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa	120
ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg	180
ggcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa	240
cctgaagact ttgcgnnta ttattgccag acctttggcc agggtacgaa agttgaaatt	300
aaacgtacg	309

<210> 57
 <211> 330
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> polynucleotide sequence of a VL domain

<400> 57

gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccggcgaa acgtgcgacc	60
ctgagctgca gagcggccca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa	120
ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg	180
ggcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa	240
cctgaagact ttgcgactta ttattgccag cagatgtcta attatcctga tacctttggc	300
cagggtacga aagttgaaat taaacgtacg	330

<210> 58
 <211> 330
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> polynucleotide sequence of a VL domain

<400> 58

gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccggcgaa acgtgcgacc	60
ctgagctgca gagcggccca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa	120
ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg	180
ggcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa	240
cctgaagact ttgcgactta ttattgccag cagactaata atgctctgt tacctttggc	300
cagggtacga aagttgaaat taaacgtacg	330

<210> 59
 <211> 324
 <212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 59

gatatcgta	tgacccagag	cccgatagc	ctggcggtga	gcctggcg	acgtgcgacc	60
attaactgca	gaagcagcca	gagcgtgctg	tatagcagca	acaacaaaaa	ctatctggcg	120
tggtaccagc	agaaaccagg	tcagccgccc	aaactattaa	tttattggc	atccacccgt	180
gaaagcgggg	tcccgatcg	ttttagccgc	tctggatccg	gcactgattt	taccctgacc	240
atttcgtccc	tgcaagctga	agacgtggcg	gtgtattatt	gccagacctt	tggccagggt	300
acgaaagttg	aaattaaacg	tacg				324

<210> 60

<211> 345

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 60

gatatcgta	tgacccagag	cccgatagc	ctggcggtga	gcctggcg	acgtgcgacc	60
attaactgca	gaagcagcca	gagcgtgctg	tatagcagca	acaacaaaaa	ctatctggcg	120
tggtaccagc	agaaaccagg	tcagccgccc	aaactattaa	tttattggc	atccacccgt	180
gaaagcgggg	tcccgatcg	ttttagccgc	tctggatccg	gcactgattt	taccctgacc	240
atttcgtccc	tgcaagctga	agacgtggcg	gtgtattatt	gccagcagta	tgattctatt	300
ccttataacct	ttggccagggt	tacgaaagtt	gaaattaaac	gtacg		345

<210> 61

<211> 315

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 61

gatatcgcac	tgacccagcc	agcttcagtg	agcggctcac	caggtcagag	cattaccatc	60
tctgtacgg	gtactagcag	cgatgtggc	ggctataact	atgtgagctg	gtaccagcag	120
catccccggg	aggcgccgaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
agcaaccgtt	ttagcggatc	caaaagccgc	aacaccgcga	gcctgaccat	tagcggcctg	240
caagcggaaag	acgaacgcga	ttattattgc	caggacgtgt	ttggcggcgg	cacgaagtta	300
accgttcttg	gccag					315

<210> 62

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 62

gatatcgcac	tgacccagcc	agcttcagtg	agcggctcac	caggtcagag	cattaccatc	60
tctgtacgg	gtactagcag	cgatgtggc	ggctataact	atgtgagctg	gtaccagcag	120
catccccggg	aggcgccgaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
agcaaccgtt	ttagcggatc	caaaagccgc	aacaccgcga	gcctgaccat	tagcggcctg	240

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caagcggaaag	acgaagcgg	ttattattgc	cagagctatg	acatgtataa	ttatattgtg	300
tttggcggcg	gcacgaagtt	aaccgttctt	ggccag			336
<210> 63						
<211> 330						
<212> DNA						
<213> Artificial Sequence						
<220>						
<223> polynucleotide sequence of a VL domain						
<400> 63						
gatatcgac	tgacccagcc	agttcagtg	agcggctcac	caggtcagag	cattaccatc	60
tcgtgtacgg	gtactagcag	cgatgtggc	ggctataact	atgtgagctg	gtaccagcag	120
catcccgaaa	aggcgccgaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
agcaaccgtt	ttagcggatc	caaagcggc	aacaccgcga	gcctgaccat	tagcggcctg	240
caagcggaaag	acgaagcgg	ttattattgc	cagtcgtatc	attttatga	ggtgtttggc	300
ggccgcacga	agttaacccgt	tcttggccag				330
<210> 64						
<211> 336						
<212> DNA						
<213> Artificial Sequence						
<220>						
<223> polynucleotide sequence of a VL domain						
<400> 64						
gatatcgac	tgacccagcc	agttcagtg	agcggctcac	caggtcagag	cattaccatc	60
tcgtgtacgg	gtactagcag	cgatgtggc	ggctataact	atgtgagctg	gtaccagcag	120
catcccgaaa	aggcgccgaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
agcaaccgtt	ttagcggatc	caaagcggc	aacaccgcga	gcctgaccat	tagcggcctg	240
caagcggaaag	acgaagcgg	ttattattgc	cagagctatg	acaataattc	tgtatgttg	300
tttggcggcg	gcacgaagtt	aaccgttctt	ggccag			336
<210> 65						
<211> 306						
<212> DNA						
<213> Artificial Sequence						
<220>						
<223> polynucleotide sequence of a VL domain						
<400> 65						
gatatcgaa	tgacccagcc	gcttcagtg	agcgttgcac	caggtcagac	cgcgcgtatc	60
tcgtgtacg	gcgtacgc	ggcgataaa	tacgcgagct	ggtaccagca	gaaaccggg	120
caggcgccag	ttctgggtat	ttatgatgat	tctgaccgtc	cctcaggcat	cccggAACgc	180
tttagcggat	ccaacagcgg	caacaccgcg	accctgacca	ttagcggcac	tcaggcggaa	240
gacgaagcgg	attattattg	ccaggacgtg	tttggcggcg	gcacgaagtt	aaccgttctt	300
ggccag						306
<210> 66						
<211> 324						
<212> DNA						
<213> Artificial Sequence						
<220>						

<223> polynucleotide sequence of a VL domain

<400> 66

gatatcgaa	tgacccagcc	gccttcagtg	agcgttgcac	caggtcagac	cgcgcgtatc	60
tcgtgtagcg	gcgatgcgct	gggcgataaa	tacgcgagct	ggtaccagca	gaaaccggg	120
caggcgccag	ttctgggtat	ttatgtat	tctgaccgtc	cctcaggcat	cccggAACgc	180
tttagcggat	ccaacagcgg	caacaccgcg	accctgacca	ttagcggcac	tcagggcggaa	240
gacgaagcgg	attattattg	ccagagctat	gactattta	agcttgcgtt	tggcggcggc	300
acgaagttaa	ccgttcttgg	ccag				324

<210> 67

<211> 327

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 67

gatatcgaa	tgacccagcc	gccttcagtg	agcgttgcac	caggtcagac	cgcgcgtatc	60
tcgtgtagcg	gcgatgcgct	gggcgataaa	tacgcgagct	ggtaccagca	gaaaccggg	120
caggcgccag	ttctgggtat	ttatgtat	tctgaccgtc	cctcaggcat	cccggAACgc	180
tttagcggat	ccaacagcgg	caacaccgcg	accctgacca	ttagcggcac	tcagggcggaa	240
gacgaagcgg	attattattg	ccagagctat	gactattctg	ctgattatgt	tttggcggc	300
ggcacgaagt	taaccgttct	tggccag				327

<210> 68

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 68

gatatcgaa	tgacccagcc	gccttcagtg	agcgttgcac	caggtcagac	cgcgcgtatc	60
tcgtgtagcg	gcgatgcgct	gggcgataaa	tacgcgagct	ggtaccagca	gaaaccggg	120
caggcgccag	ttctgggtat	ttatgtat	tctgaccgtc	cctcaggcat	cccggAACgc	180
tttagcggat	ccaacagcgg	caacaccgcg	accctgacca	ttagcggcac	tcagggcggaa	240
gacgaagcgg	attattattg	ccagagctat	gactttgatt	ttgctgtgtt	tggcggcggc	300
acgaagttaa	ccgttcttgg	ccag				324

<210> 69

<211> 327

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VL domain

<400> 69

gatatcgaa	tgacccagcc	gccttcagtg	agcgttgcac	caggtcagac	cgcgcgtatc	60
tcgtgtagcg	gcgatgcgct	gggcgataaa	tacgcgagct	ggtaccagca	gaaaccggg	120
caggcgccag	ttctgggtat	ttatgtat	tctgaccgtc	cctcaggcat	cccggAACgc	180
tttagcggat	ccaacagcgg	caacaccgcg	accctgacca	ttagcggcac	tcagggcggaa	240
gacgaagcgg	attattattg	ccagagctat	gacggtcctg	atctttgggt	tttggcggc	300
ggcacgaagt	taaccgttct	tggccag				327

<210> 70
 <211> 332
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> polynucleotide sequence of a VH domain

 <220>
 <221> misc_feature
 <222> (1)...(3)
 <223> NNN=GAA OR CAG

 <400> 70

nnngtcaat	tggttcagtc	tggcgcgaa	gtaaaaaaac	cgggcagcag	cgtaaaagt	60
agctgcaaag	cctccggagg	cacttttagc	agctatgcga	ttagctgggt	gcccagcc	120
cctggcagg	gtctcgagt	gatgggcggc	attattccga	tttttggcac	ggcgaactac	180
gcccagaagt	ttcagggccg	ggtgaccatt	accgcggatg	aaagcaccag	caccgcgtat	240
atggaactga	gcagcctg	tagcgaagat	acggccgtgt	attattgcgc	gcgtgattgg	300
ggccaaggca	ccctggtgac	ggttagctca	gc			332

<210> 71
 <211> 359
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> polynucleotide sequence of a VH domain

 <400> 71

caggtcaat	tggttcagtc	tggcgcgaa	gtaaaaaaac	cgggcagcag	cgtaaaagt	60
agctgcaaag	cctccggagg	cacttttagc	agctatgcga	ttagctgggt	gcccagcc	120
cctggcagg	gtctcgagt	gatgggcggc	attattccga	tttttggcac	ggcgaactac	180
gcccagaagt	ttcagggccg	ggtgaccatt	accgcggatg	aaagcaccag	caccgcgtat	240
atggaactga	gcagcctg	tagcgaagat	acggccgtgt	attattgcgc	gcgtgataat	300
tggtaa	cttttctga	tgtttgggc	caaggcaccc	tggtgacgg	tagctcagc	359

<210> 72
 <211> 359
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> polynucleotide sequence of a VH domain

 <400> 72

caggtcaat	tggttcagtc	tggcgcgaa	gtaaaaaaac	cgggcagcag	cgtaaaagt	60
agctgcaaag	cctccggagg	cacttttagc	agctatgcga	ttagctgggt	gcccagcc	120
cctggcagg	gtctcgagt	gatgggcggc	attattccga	tttttggcac	ggcgaactac	180
gcccagaagt	ttcagggccg	ggtgaccatt	accgcggatg	aaagcaccag	caccgcgtat	240
atggaactga	gcagcctg	tagcgaagat	acggccgtgt	attattgcgc	gcgtgttaat	300
cattggactt	atactttga	ttattgggc	caaggcaccc	tggtgacgg	tagctcagc	359

<210> 73
 <211> 374
 <212> DNA

<220>

<223> polynucleotide sequence of a VH domain

<400> 76

caggtgcaat	tggttcagag	cggcgcggaa	gtaaaaaac	cgggcgcgag	cgtaaaagt	60
agctgcaaag	cctccggata	taccttacc	agctattata	tgcactgggt	ccgccaagcc	120
cctggcagg	gtctcgagt	gatgggctgg	attaaccga	atagcggcgg	cacgaactac	180
gcccagaagt	ttcagggccg	ggtgaccatg	accctgtata	ccagcattag	caccgcgtat	240
atggaactga	gcagcctg	tagcgaagat	acggccgtgt	attattgcgc	gcgttctatg	300
aattctacta	tgtattggta	tcttcgtcgt	gttcttttg	atcattgggg	ccaaggcacc	360
ctgggtacgg	ttagctcagc					380

<210> 77

<211> 356

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VH domain

<400> 77

caggtgcaat	tggttcagag	cggcgcggaa	gtaaaaaac	cgggcgcgag	cgtaaaagt	60
agctgcaaag	cctccggata	taccttacc	agctattata	tgcactgggt	ccgccaagcc	120
cctggcagg	gtctcgagt	gatgggctgg	attaaccga	atagcggcgg	cacgaactac	180
gcccagaagt	ttcagggccg	ggtgaccatg	accctgtata	ccagcattag	caccgcgtat	240
atggaactga	gcagcctg	tagcgaagat	acggccgtgt	attattgcgc	gcgtgatttt	300
cttggttatg	agtttgatta	ttggggccaa	ggcacccctgg	tgacggttag	ctcagc	356

<210> 78

<211> 380

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VH domain

<400> 78

caggtgcaat	tggttcagag	cggcgcggaa	gtaaaaaac	cgggcgcgag	cgtaaaagt	60
agctgcaaag	cctccggata	taccttacc	agctattata	tgcactgggt	ccgccaagcc	120
cctggcagg	gtctcgagt	gatgggctgg	attaaccga	atagcggcgg	cacgaactac	180
gcccagaagt	ttcagggccg	ggtgaccatg	accctgtata	ccagcattag	caccgcgtat	240
atggaactga	gcagcctg	tagcgaagat	acggccgtgt	attattgcgc	gcgttattat	300
gtttcttctc	tttatcatta	tgttttgg	gtttttattg	attattgggg	ccaaggcacc	360
ctgggtacgg	ttagctcagc					380

<210> 79

<211> 380

<212> DNA

<213> Artificial Sequence

<220>

<223> polynucleotide sequence of a VH domain

<400> 79

caggtgcaat	tggttcagag	cggcgcggaa	gtaaaaaac	cgggcgcgag	cgtaaaagt	60
agctgcaaag	cctccggata	taccttacc	agctattata	tgcactgggt	ccgccaagcc	120
cctggcagg	gtctcgagt	gatgggctgg	attaaccga	atagcggcgg	cacgaactac	180
gcccagaagt	ttcagggccg	ggtgaccatg	accctgtata	ccagcattag	caccgcgtat	240

atggaactga	gcagcctg	cg tagcgaagat acggccgtgt	attattgcgc	gcgtggttat	300	
tgttatgctt	atttactta	tattaattat gttattttg	ataattgggg	ccaaggcacc	360	
ctggta	cgg	ttagctcagc			380	
<210>	80					
<211>	383					
<212>	DNA					
<213>	Artificial Sequence					
<220>						
<223>	polynucleotide sequence of a VH domain					
<400>	80					
caggtgcaat	tggttcagag	cggcgcgaa	gtgaaaaaac	cgggcgcgag	cgtaaaagt	60
actgtcaa	ag	cctccggata	taccttacc	agctattata	tgcactgggt	120
cctggcagg	gtctcgagt	gtgggcgtgg	attaacccga	atagcggcgg	cacgaactac	180
gcccaga	ttcagggccc	ggtgaccatg	accctgtata	ccagcattag	caccgcgtat	240
atggaactga	gcagcctg	cg tagcgaagat	acggccgtgt	attattgcgc	gcgtacttgg	300
cagtattctt	attttatta	tcttgcgtgt	gttattattt	ttgatattt	ggccaaggc	360
accctggta	cggtagctc	agc				383
<210>	81					
<211>	335					
<212>	DNA					
<213>	Artificial Sequence					
<220>						
<223>	polynucleotide sequence of a VH domain					
<220>						
<221>	misc_feature					
<222>	(1)..(3)					
<223>	NNN=GAA OR CAG					
<400>	81					
nnngtcaat	tgaaagaaag	cggccggcc	ctggtaaaac	cgacccaa	cctgaccctg	60
acctgtac	tttccggatt	tagcctgtcc	acgtctggcg	ttggcgtgg	ctggattcgc	120
cagccctg	ggaaagccct	cgagtggctg	gctctgattg	attggatga	tgataagtat	180
tatagcacca	gcctgaaaac	gcgtctgacc	attagcaaag	atacttcgaa	aaatcaggtg	240
gtgctgacta	tgaccaacat	ggacccggtg	gatacggcca	cctattattt	cgcgcgtat	300
tggggccaag	gcaccctgg	gacggtagc	tcagc			335
<210>	82					
<211>	392					
<212>	DNA					
<213>	Artificial Sequence					
<220>						
<223>	polynucleotide sequence of a VH domain					
<400>	82					
caggtgcaat	tgaaagaaag	cggccggcc	ctggtaaaac	cgacccaa	cctgaccctg	60
acctgtac	tttccggatt	tagcctgtcc	acgtctggcg	ttggcgtgg	ctggattcgc	120
cagccctg	ggaaagccct	cgagtggctg	gctctgattt	attggatga	tgataagtat	180
tatagcacca	gcctgaaaac	gcgtctgacc	attagcaaag	atacttcgaa	aaatcaggtg	240
gtgctgacta	tgaccaacat	ggacccggtg	gatacggcca	cctattattt	cgcgcgtat	300
cattcttgg	atgagatgg	ttattatgg	tctactgtt	gttataatgtt	tgattatttgg	360

ggccaaggca ccctggtgac ggttagctca gc

392

<210> 83
 <211> 341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> polynucleotide sequence of a VH domain

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> NNN=GAA OR CAG

<400> 83
 nnngtcaat tgcaaacagtc tggtccgggc ctggtaaaac cgagccaaac cctgagcctg 60
 acctgtgcga tttccggaga tagcgtgagc agcaacagcg cggcgtggaa ctggattcgc 120
 cagtctcctg ggcgtggcct cgagtggctg ggcgttacct attatcgttag caaatggtat 180
 aacgattatg cggtgagcgt gaaaagccgg attaccatca acccgatata ttcgaaaaac 240
 cagtttagcc tgcaactgaa cagcgtgacc ccgaaagata cggccgtgta ttattgcgcg 300
 cgtgattggg gccaaggcac cctggtaac gttagctac c 341

<210> 84
 <211> 362
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> polynucleotide sequence of a VH domain

<400> 84
 caggtgcaat tgcaaacagtc tggtccgggc ctggtaaaac cgagccaaac cctgagcctg 60
 acctgtgcga tttccggaga tagcgtgagc agcaacagcg cggcgtggaa ctggattcgc 120
 cagtctcctg ggcgtggcct cgagtggctg ggcgttacct attatcgttag caaatggtat 180
 aacgattatg cggtgagcgt gaaaagccgg attaccatca acccgatata ttcgaaaaac 240
 cagtttagcc tgcaactgaa cagcgtgacc ccgaaagata cggccgtgta ttattgcgcg 300
 cgttcttatt atcctgattt tgattattgg gccaaggca ccctggtaac gttagctca 360
 gc 362

<210> 85
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> polypeptide sequence of a VL domain

<400> 85

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1 5 10 15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
 20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr

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35

40

45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Ser Ala Asp Tyr
85 90 95

Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105

<210> 86
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 86

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser His His Phe Tyr
85 90 95

Glu Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

<210> 87
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 87

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala

20

25

30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Asp Phe Ala Val
 85 90 95

Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105

<210> 88

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VL domain

<400> 88

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
 85 90 95

Tyr Asp Ser Ile Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
 100 105 110

Lys Arg Thr
 115

<210> 89

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VL domain

<400> 89

Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1					5					10					15
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser
															30
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
															45
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser
															60
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu
															80
Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Met	Ser	Asn	Tyr	Pro
															95
Asp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr		
															110

<210> 90

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VL domain

<400> 90

Asp	Ile	Ala	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln
1					5					10					15
Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Gly	Tyr
															30
Asn	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu
															45
Met	Ile	Tyr	Asp	Val	Ser	Asn	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe
															50
Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu
															65
Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Tyr	Asp	Asn	Asn
															85
Ser	Asp	Val	Val	Phe	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	
															100
															105
															110

<210> 91

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VL domain

<400> 91

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Ser	Tyr
	20				25							30			

Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
	35				40							45			

Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50				55						60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65				70				75					80		

Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Phe	Gln	Tyr	Gly	Ser	Ile	Pro	Pro
	85					90						95			

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr			
	100					105									

<210> 92

<211> 110

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VL domain

<400> 92

Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	

Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser
	20				25							30			

Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
	35				40							45			

Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser
	50				55							60			

Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu
65				70				75					80		

Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Thr	Asn	Asn	Ala	Pro
	85				90							95			

Val	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr		
	100					105						110			

<210> 93

<211> 108

<212> PRT
 <213> Artificial Sequence

<220>
 <223> polypeptide sequence of a VL domain

<400> 93

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1 5 10 15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
 20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Phe Lys Leu Val
 85 90 95

Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105

<210> 94
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> polypeptide sequence of a VL domain

<400> 94

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Tyr
 85 90 95

Asn Tyr Ile Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110

<210> 95
 <211> 109
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> polypeptide sequence of a VL domain
 <400> 95

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1 5 10 15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
 20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Gly Pro Asp Leu Trp
 85 90 95

Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105

<210> 96
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> polypeptide sequence of a VH domain
 <400> 96

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Phe Leu Gly Tyr Glu Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 97
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> polypeptide sequence of a VH domain

<400> 97

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Gly Ser Ser Leu Tyr His Tyr Val Phe Gly Gly Phe
 100 105 110

Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 98
 <211> 130
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> polypeptide sequence of a VH domain

<400> 98

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
 50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Tyr His Ser Trp Tyr Glu Met Gly Tyr Tyr Gly Ser Thr
 100 105 110

Val Gly Tyr Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
 115 120 125

Ser Ser
 130

<210> 99
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> polypeptide sequence of a VH domain

<400> 99

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Asn Trp Phe Lys Pro Phe Ser Asp Val Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 100
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> polypeptide sequence of a VH domain

<400> 100

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1					5					10			15		

Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr
						20			25			30			

Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
					35			40			45				

Gly	Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe
					50			55			60				

Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	Thr	Ala	Tyr
					65			70		75			80		

Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
					85			90		95					

Ala	Arg	Val	Asn	His	Trp	Thr	Tyr	Thr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly
					100			105			110				

Thr	Leu	Val	Thr	Val	Ser	Ser									
					115										

<210> 101

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VH domain

<400> 101

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1					5					10			15		

Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
					20			25		30					

Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
					35			40			45				

Gly	Trp	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe
					50			55		60					

Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr
					65			70		75			80		

Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
					85			90		95					

Ala	Arg	Gly	Tyr	Trp	Tyr	Ala	Tyr	Phe	Thr	Tyr	Ile	Asn	Tyr	Gly	Tyr
					100			105		110					

Phe	Asp	Asn	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
					115			120		125					

<210> 102
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> polypeptide sequence of a VH domain
 <400> 102

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Gly Trp Val Ser His Gly Tyr Tyr Tyr Leu Phe Asp
 100 105 110

Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 103
 <211> 127
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> polypeptide sequence of a VH domain

<400> 103

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Thr Trp Gln Tyr Ser Tyr Phe Tyr Tyr Leu Asp Gly Gly Tyr
 100 105 110

Tyr Phe Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 104

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VH domain

<400> 104

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asn Met Ala Tyr Thr Asn Tyr Gln Tyr Val Asn Met Pro His
 100 105 110

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 105

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VH domain

<400> 105

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Ser Met Asn Ser Thr Met Tyr Trp Tyr Leu Arg Arg Val Leu
 100 105 110

Phe Asp His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 106

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VH domain

<400> 106

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
 20 25 30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
 35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
 50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
 65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
 85 90 95

Tyr Tyr Cys Ala Arg Ser Tyr Tyr Pro Asp Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120